

AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph beginning at page 18, line 11 with the following amended paragraph.

An alignment of the protein sequences encoded by the DNAs with the gp120 amino acid sequence of HXB2, a prototype CD4-tropic isolate, and the closest published gp120 amino acid sequence, WEAU1.6, is presented in Figure 4. In the figure, dashes signify 100% identity among sequences and dots signify the absence/deletion of a base. Differences between AD3.v6/AD3.v22 viruses and WEAU1.6 are colored red in the WEAU1.6 sequence. Figure 4 displays the gp120 polypeptide and clearly indicates the location of the V1, V2, V3, V4 and V5 loops.

Please replace the paragraph beginning at page 18, line 17 with the following amended paragraph.

Extensive differences exist throughout AD3.v6 and AD3.v22 gp120 when compared with HXB2 and with WEAU1.6. The changes were most extensive in variable (V) loops and a striking feature of these changes was an extended V1-V2 loop. Extensive differences were also present in the important V3 loop when compared to its closest match. In contrast, only a single point change was observed in the entire gp41 between AD3.v6 and AD3.v22 viruses (not shown). Interestingly, the CD4 binding region (~~in blue~~) and other residues that are known to be important for CD4-tropism (~~underlined~~) remained unchanged.